



Supplement of

Alterations in microbial community composition with increasing $f\text{CO}_2$: a mesocosm study in the eastern Baltic Sea

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Table S1. Viral lysis rates (d^{-1}) of the phytoplankton groups detected by flow cytometry in M1 (low fCO_2) and M3 (high fCO_2), as determined by dilution assays performed on the days specified. Lysis rates are calculated as total loss rates (from 30 KDa dilutions) minus grazing rates (from 0.45 μm dilutions). Significant lysis specified as $p \leq 0.05$ is marked with an asterisk. A zero means no lysis was detected, no data denotes a failed experiment.

Rate d^{-1}												
Mesocosm 1							Mesocosm 3					
Day	Syn	Pico I	Pico II	Pico III	Nano I	Nano II	Syn	Pico I	Pico II	Pico III	Nano I	Nano II
1				-0.09			0	-0.09	-0.03	0		-0.1
3	0	-0.09				-0.61		-0.11 *			-0.21	
6		0	-0.35						-0.43 *		-0.76 *	
10	0	-0.02	0	0	0	-0.01		-0.21 *	-0.12		-0.13	-0.02
13	0		0	0	-0.23 *	-0.45		-0.14 *	-0.55 *		-0.19	-0.34
17	0				0		-0.12	-0.15 *	-0.01		-0.08	0
20									0		-0.34	-1.05 *
24		-0.06		0		0		-0.02	0		-0.35	
31	-0.01	-0.11	-0.02		0		-0.07	-0.11 *	-0.24 *		-0.27	

Fig. S1. Time-series plot of depth-integrated whole water column (0.3–17 m) abundances of **(a)** *Synechococcus* (SYN) **(b)** picoeukaryotes I (Pico-I) **(c)** picoeukaryotes II (Pico-II) **(d)** picoeukaryotes III (Pico-III) **(e)** nanoeukaryotes I (Nano-I) **(f)** nanoeukaryotes II (Nano-II) **(g)** Total heterotrophic prokaryotes, **(h)** High nucleic acid heterotrophic prokaryotes (HNA), **(i)** Low nucleic acid heterotrophic prokaryotes (LNA), **(j)** Total virus, distinguished by flow cytometric analysis of each mesocosm community and in the surrounding waters (Baltic). Dotted lines indicate the end of Phase I and end of Phase II.

Fig. S2. Correlation plots of net growth rate against temporally averaged $f\text{CO}_2$ for NMDS-based period 1 (days 3-13) for the different microbial groups distinguished by flow cytometry: **(a)** SYN, **(b)** Pico-I, **(c)** Pico-II, **(d)** Pico-III, **(e)** Nano-I, **(f)** Nano-II, **(g)** LNA prokaryotes, and **(h)** HNA Prokaryotes. A negative growth rate indicates a net loss of cells.

Fig. S3. Correlation plots of net growth rate against temporally averaged $f\text{CO}_2$ for NMDS-based period 2 (days 16-24) for the different microbial groups distinguished by flow cytometry: **(a)** SYN, **(b)** Pico-I, **(c)** Pico-II, **(d)** Pico-III, **(e)** Nano-I, **(f)** Nano-II, **(g)** LNA prokaryotes, and **(h)** HNA Prokaryotes. A negative growth rate indicates a net loss of cells.

Fig. S4. Correlation plots of abundance versus actual $f\text{CO}_2$ for different phytoplankton groups on specified days: **(a)** SYN on day 24, **(b)** Pico-I on day 5, **(c)** day 13 and **(d)** day 21, **(e)** Pico-II on day 17, **(f)** Pico-III on day 24, **(g)** Nano-I on day 17 and **(h)** Nano-II on day 17.

Fig. S5. Correlation plots of net growth rates versus temporally averaged $f\text{CO}_2$ over specified periods: **(a)** Pico I on days 1-5, and **(b)** days 5-9, **(c)** Pico-II between days 12-17. A negative growth rate indicates a net loss of cells.

Fig. S6. Time-series plot of depth-integrated whole water column (0.3–10 m) abundances of **(a)** nanophytoplankton I and **(b)** nanophytoplankton II to show total abundances in Baltic Sea, surrounding water samples. Dotted lines indicate the end of Phase I and end of Phase II. Colours and symbols are the same as for Fig. S1.

Fig. S7. Time series plot of carbon biomass ($\mu\text{mol L}^{-1}$) in top (0-10 m) for **(a)** Pico-III, **(b)** Nano-I and -II combined, **(c)** total phytoplankton enumerated by flow cytometry. Dotted lines indicate the end of Phase I and end of Phase II. Carbon biomass was calculated from mean cell abundances assuming the cells to be spherical and applying conversion factors of $237 \text{ fg C } \mu\text{m}^{-3}$ (Worden et al. 2004) and $196.5 \text{ fg C } \mu\text{m}^{-3}$ (Garrison et al. 2000) for pico- and nano-sized plankton based on the average cell diameters.

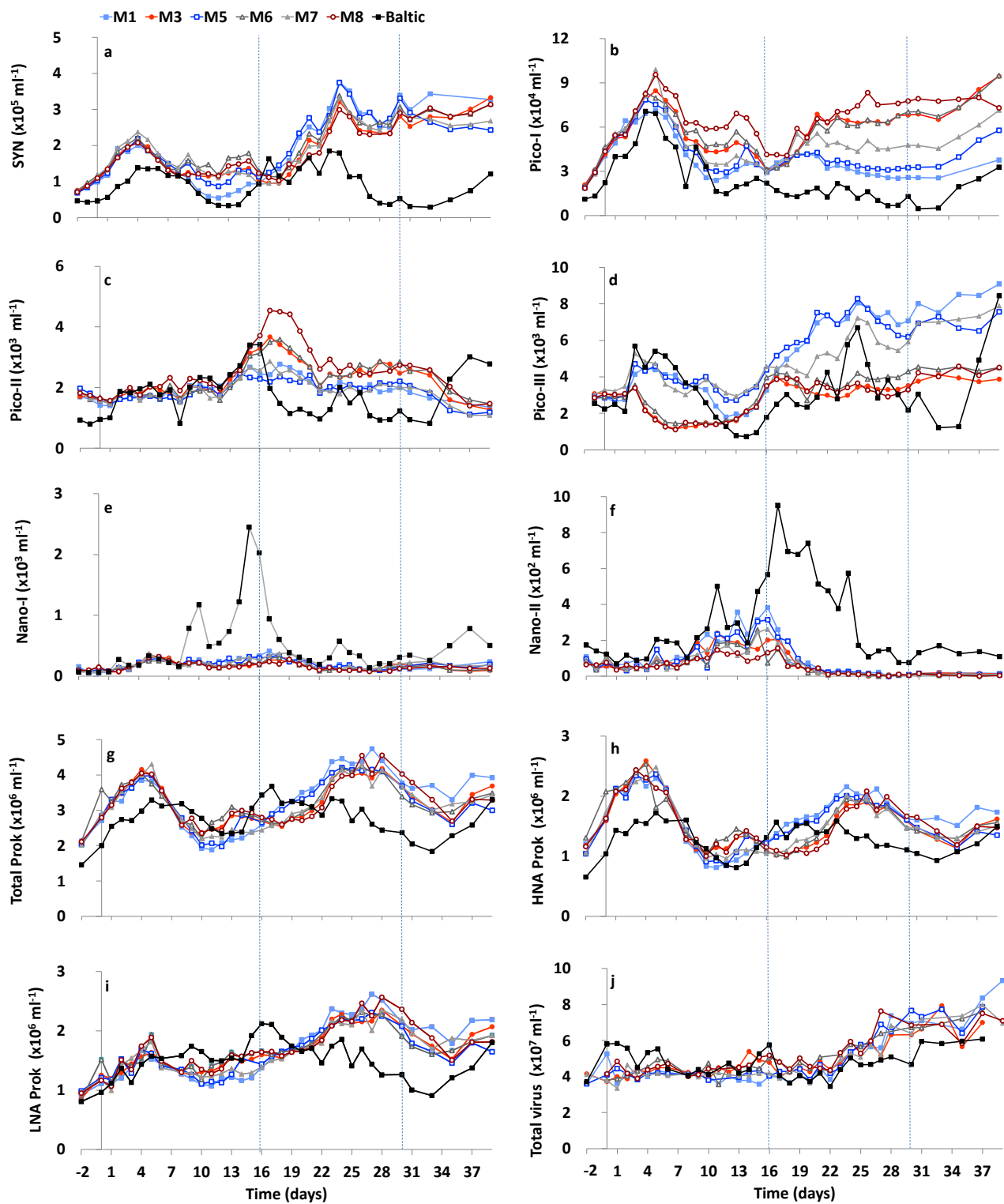


Figure S1.

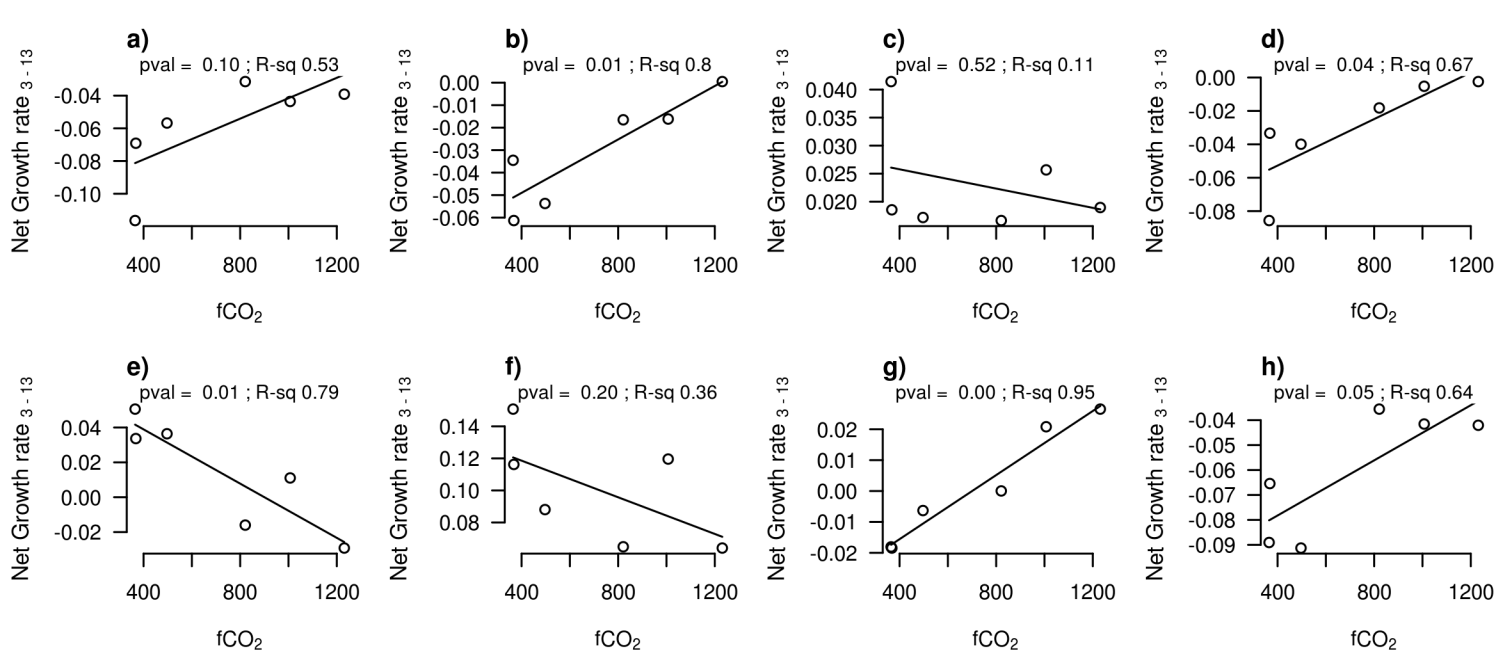


Figure S2.

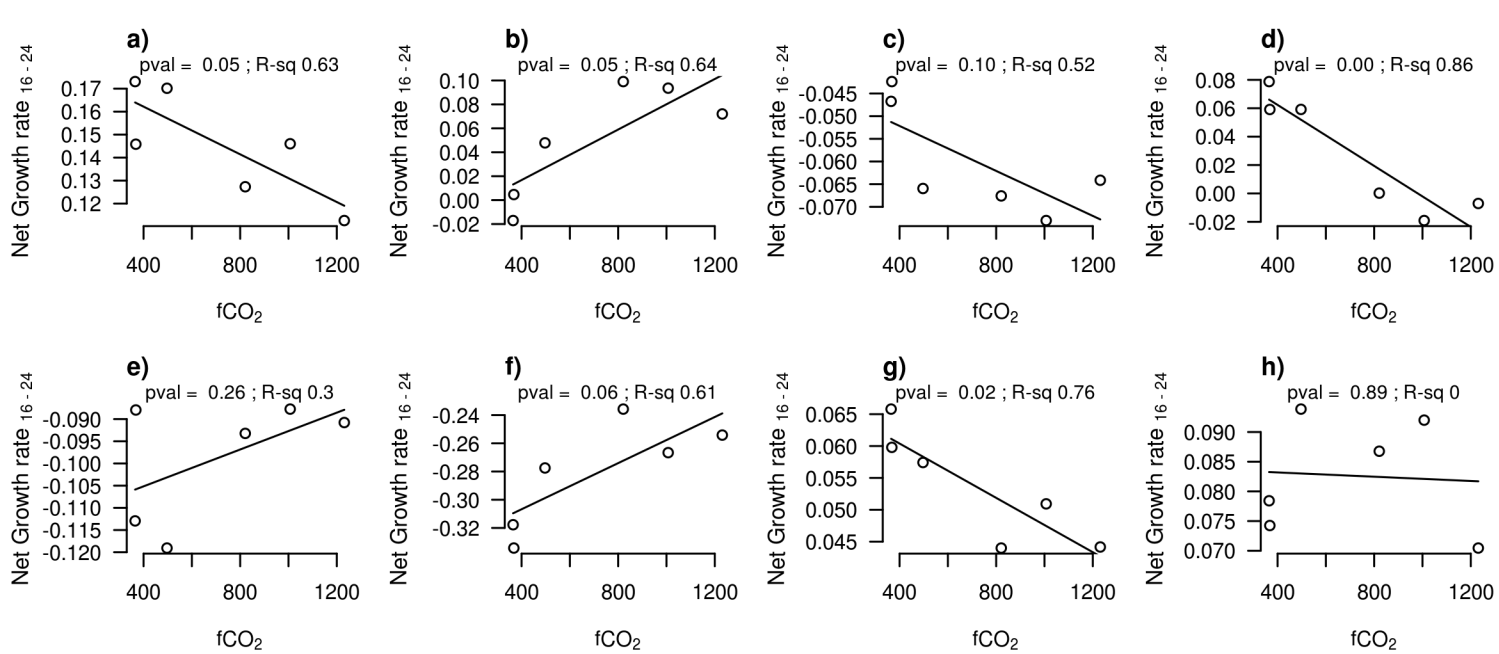


Figure S3.

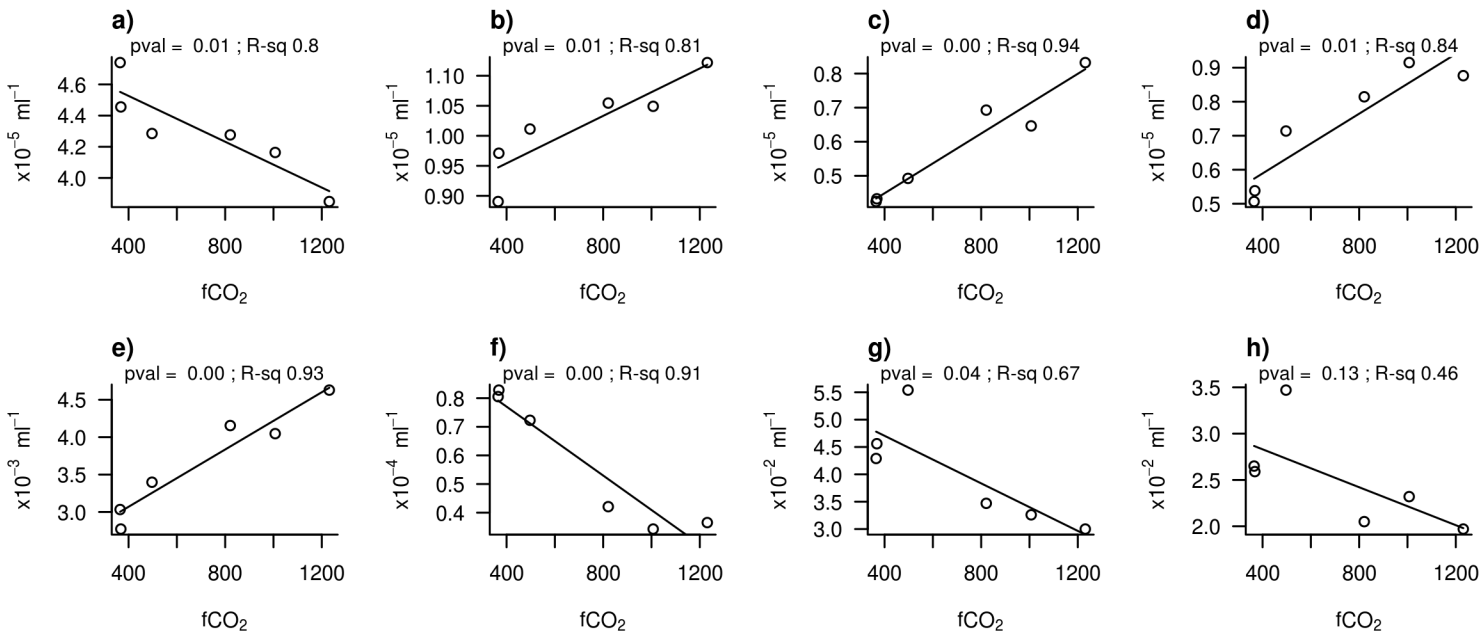


Figure S4.

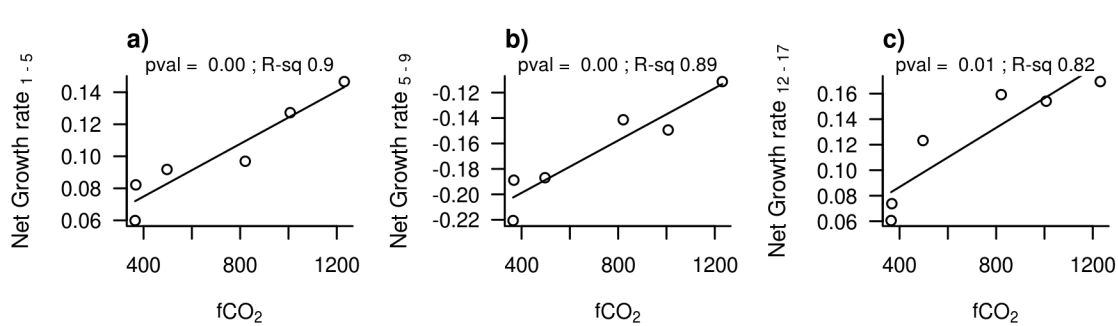


Figure S5.

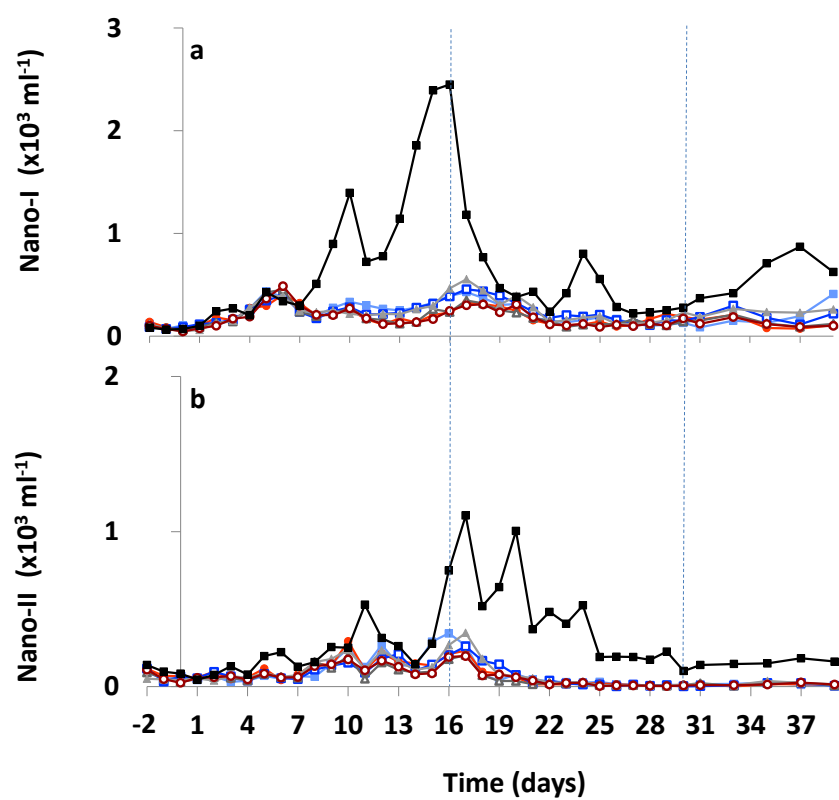


Figure S6.

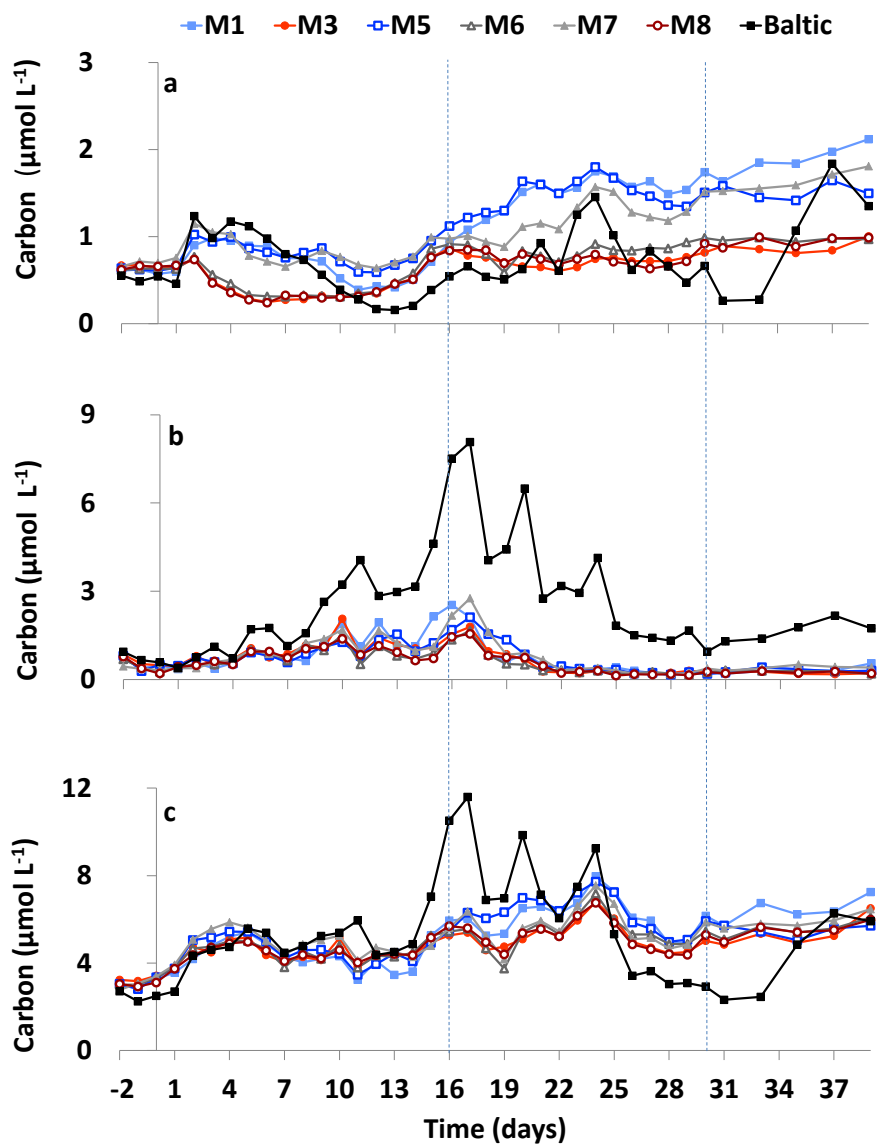


Figure S7.